Transgenic Plants

Reference to Related Applications

This application claims priority to U.S. Provisional Application 60/3449,054 filed February 22, 2003, incorporated herein by reference in its entirety.

Incorporation Of Sequence Listing

The sequences in the enclosed Sequence Listing are identical to the sequences in the Sequence Listing and computer readable form of prior U.S. Provisional Application 60/3449,054 filed February 22, 2003, which contain the file named "G1073FINAL.ST25.txt" which is 21 kb and was created on 21 Feb 2003 and which is incorporated herein by reference.

Field of the Invention

Disclosed herein are DNA useful for producing transgenic plants and seeds and methods of making and using such transgenic plants and seed.

Background Of The Invention

Water deficit can have adverse effects on plants such as yield reductions, increased susceptibility to disease and pests, reduced plant growth and reproductive failure. An object of this invention is to provide plants which can express genes to ameliorate the adverse effects of water deficit. Useful genes for expression especially during water deficit are genes which promote aspects of plant growth or fertility, genes which impart disease resistance, genes which impart pest resistance, and the like.

Considering the complexity of water use in land plants, especially during conditions that produce water deficit, relatively few genes specifically associated with this aspect of physiology have been identified. It would be of benefit to the art to increase the number and variety of genes involved in regulating water use in plants, more particularly, in corn plants, and even more particularly in corn plants experiencing water deficit. It would be especially advantageous to identify transcription factors which can be used in directing the production of proteins which are beneficial to the plant when produced during water deficit.

Transcription factors are investigated for improving plant properties and traits in transgenic plants. Reference is made to WO 02079403 of Mendel Biotechnology, Inc. which

claims priority from U.S. application Serial No. 09/823,676 (incorporated herein by reference) for a disclosure of a variety of *Arabidopsis thaliana* transcription factors including one identified as G1073 which are alleged to be useful for modifying plant biomass, for methods of building DNA constructs which express transcript factors, and for methods of producing transformed plants with DNA constructs which express transcription factors.

One of the goals of plant genetic engineering is to produce plants with agronomically, horticulturally or economically important traits including tolerance to any of a variety of environmental stresses such as water deficit. Many transgenic crop plants have recombinant DNA that confers herbicide and/or pest resistance traits. Incorporation of additional recombinant DNA for conferring crop improvement traits in crop plants presents a challenge of using DNA constructs of increased complexity.

Summary of the Invention

We have discovered that transcription factors G1073 and homologs (G1073 transcription factors) are useful for imparting enhanced resistance and/or tolerance to water deficit in transgenic plants. The present invention is directed to DNA which encode at least a functional part of a G1073 transcription factor which is useful in transgenic plants for enhancing yield when the plants are subjected to water deficit. One aspect of this invention provides methods for providing transgenic plants with an enhanced resistance and/or tolerance to water deficit. More particularly the method comprises transforming plants with recombinant DNA construct comprising DNA which encodes at least a functional part of a G1073 transcription factor, e.g. which imparts resistance to and/or tolerance to water deficit. Another aspect of the invention provides transgenic seed for growing a plant which is resistant to water deficit as compared to wild type wherein the genome of said seed comprises recombinant DNA which expresses at least a functional part of such a G1073 transcription factor, e.g. having an amino acid sequence comprising at least 50 contiguous amino acids of a G1073 transcription factor. In another aspect of the invention such transgenic seed has in its genome recombinant DNA which expresses a transcription factor polypeptide having an amino acid sequences which is at least 50% identical (and preferably of higher identity) with a synthetic consensus amino acid sequence from a conserved region of a G1073 transcription factor. In one aspect of the invention the recombinant DNA is exogenous DNA. In another aspect of the invention the DNA expressing a G1073 transcription factor is DNA from the *Arabidopsis thaliana* transcription factor G1073. In yet

another aspect of the invention the DNA expressing a G1073 transcription factor is not derived from the *Arabidopsis thaliana* transcription factor G1073, but rather is derived from DNA expressing a homologous G1073 transcription factor from another species.

This invention also provides plants grown from such transgenic seed with recombinant DNA expressing a G1073 transcription factor. Transformed plants with tolerance and/or resistance to water deficit should inherently provide enhanced yield as compared to wild type plants which are stunted by or succumb to water deficit. One aspect of the invention provides transgenic plants with stacked engineered traits, e.g. a crop improvement trait provided by recombinant DNA expressing a G1073 transcription factor in combination with herbicide and/or pest resistance traits.

Another aspect of the invention provides hybrid corn with stacked engineered traits. One embodiment of such hybrid corn is the progeny of a transgenic ancestor corn plant having in its genome a recombinant DNA which expresses a G1073 transcription factor in combination with an herbicide and/or pest resistance trait. Embodiments of such hybrid corn have a transgenic male ancestor corn plant which has in its genome recombinant DNA which confers herbicide resistance and/or pest resistance.

Brief Description Of The Drawings

Figure 1 is an amino acid sequence alignment.

Detailed Description Of The Invention

As used herein a "G1073 transcription factor" means a protein which is expressed by DNA of SEQ ID NO:4-6 and a protein having the amino acid sequence of SEQ ID NO:1-3 and a protein having the conserved amino acid sequence of SEQ ID NO:7-10 and a protein having the consensus amino acid sequence of SEQ ID NO:11 and a homologue protein from another species and parts of such proteins that function to provide the water-deficit-tolerance trait exhibited in *Arabidopsis thaliana*, e.g. in the assay illustrated in the example below.

As used herein "water deficit" is a plant condition characterized by water potential in a plant tissue of less than –0.7 megapascals (MPa), e.g. –0.8 Mpa. Water potential in maize is conveniently measured by clamping a leaf segment in a pressurizable container so that a cut cross section of leaf is open to atmospheric pressure. Gauge pressure (above atmospheric pressure) on the contained leaf section is increased until water begins to exude from the atmospheric-pressure-exposed cross section; the gauge pressure at incipient water exudation is

reported as negative water potential in the plant tissue, e.g. 7 bars of gauge pressure is reported as -0.7 MPa water potential. Water deficit can be induced by withholding water from plants for sufficient time that wild type plants are deleteriously affected, e.g. as manifested by reduced yield, stunted growth, retarded development, death or the like. The plants of this invention show a remarkable risibility after periods of water deficit that are adverse to wild type plants.

As used herein "yield" of a crop plant means the production of a crop, e.g. shelled corn kernels or soybean or cotton fiber, per unit of production area, e.g. in bushels per acre or metric tons per hectare, often reported on a moisture adjusted basis, e.g. corn is typically reported at 15.5 % moisture. Moreover a bushel of corn is defined by law in the State of Iowa as 56 pounds by weight, a useful conversion factor for corn yield is: 100 bushels per acre is equivalent to 6.272 metric tons per hectare. Other measurements for yield are in common practice.
As used herein a "transgenic" organism, e.g. plant or seed, is one whose genome has been altered by the incorporation of exogenous genetic material or additional copies of native genetic material, e.g. by transformation or recombination of the organism or an ancestor organism. Transgenic plants include progeny plants of an original plant derived from a transformation process including progeny of breeding transgenic plants with wild type plants or other transgenic plants Crop plants of interest in the present invention include, but are not limited to soy, cotton, canola, maize, wheat, sunflower, sorghum, alfalfa, barley, millet, rice, tobacco, fruit and vegetable crops, and turfgrass.

As used herein an "herbicide resistance" trait is a characteristic of a transgenic plant that is resistant to dosages of an herbicide that is typically lethal to a progenitor plant. Such herbicide resistance can arise from a natural mutation or more typically from incorporation of recombinant DNA that confers herbicide resistance. Herbicides for which resistance is useful in a plant include glyphosate herbicides, phosphinothricin herbicides, oxynil herbicides, imidazolinone herbicides, dinitroaniline herbicides, pyridine herbicides, sulfonylurea herbicides, bialaphos herbicides, sulfonamide herbicides and gluphosinate herbicides. To illustrate the that production of transgenic plants with herbicide resistance is a capability of those of ordinary skill in the art reference is made to U.S. patent application publications 2003/0106096A1 and 2002/0112260A1 and U.S. Patents 5,034,322; 6,107,549 and 6,376,754, all of which are incorporated herein by reference.

As used herein an "pest resistance" trait is a characteristic of a transgenic plant is resistant to attack from a plant pest such as a virus, a nematode, a larval insect or an adult insect that typically is capable of inflicting crop yield loss in a progenitor plant. Such pest resistance can arise from a natural mutation or more typically from incorporation of recombinant DNA that confers pest resistance. For insect resistance, such recombinant DNA can, for example, encode an insect lethal protein such as a delta endotoxin of *Bacillus thuringiensis* bacteria or be transcribed to a dsRNA targeted for suppression of an essential gene in the insect. To illustrate that the production of transgenic plants with pest resistance is a capability of those of ordinary skill in the art reference is made to U.S. Patents 5,250,515 and 5,880,275 which disclose plants expressing an endotoxin of *Bacillus thuringiensis* bacteria, to U.S. Patent 6,506,599 which discloses control of invertebrates which feed on transgenic plants which express dsRNA for suppressing a target gene in the invertebrate, to U.S. Patent 5,986,175 which discloses the control of viral pests by transgenic plants which express viral replicase, and to U.S. Patent Application Publication 2003/0150017 A1 which discloses control of pests by a transgenic plant which express a dsRNA targeted to suppressing a gene in the pest, all of which are incorporated herein by reference.

SEQ ID NO: 1 provides the amino acid sequence of *Arabidopsis thaliana* transcription factor G1073, which are disclosed in U.S. application Serial No 09/823,676, filed March 26, 2001, incorporated herein by reference.

SEQ ID NO:2 provides the amino acid sequence of part of the rice (*Oryza sativa*) polypeptide which is a homolog of the *Arabidopsis thaliana* G1073 transcription factor.

SEQ ID NO:3 provides the amino acid sequence of part of the cotton (*Gossypium hirsutum*) polypeptide which is a homolog of the *Arabidopsis thaliana* G1073 transcription factor.

SEQ ID NO:4 provides DNA from the gene encoding an *Arabidopsis thaliana* G1073 transcription factor of SEQ ID NO:1.

SEQ ID NO:5 provides DNA from the gene encoding a rice transcription factor of SEQ ID NO:2.

SEQ ID NO:6 provides DNA from the gene encoding a cotton transcription factor of SEQ ID NO:3.

SEQ ID NO:7 provides a conserved region of the amino acid sequence of the *Arabidopsis thaliana* transcription factor G1067 which is disclosed in U.S. application Serial No 09/934,455, incorporated herein by reference.

SEQ ID NO: 8 provides a conserved region of the amino acid sequence of the *Arabidopsis thaliana* transcription factor G1073 (SEQ ID NO:1).

SEQ ID NO:9 provides a conserved region of the amino acid sequence of the cotton transcription factor (SEQ ID NO:2).

SEQ ID NO:10 provides a conserved region of the amino acid sequence of the rice transcription factor (SEQ ID NO:3).

SEQ ID NO:11 is an synthetic consensus amino acid sequence developed from alignment of the conserved region of SEQ ID NO: 7 through 10. The alignment is illustrated in Figure 1.

SEQ ID NO: 12 provides DNA from the gene encoding an *Arabidopsis thaliana* G1067 transcription factor, a conserved region of which is SEQ ID NO:7.

Polynucleotides of the present invention are DNA that is used to impart the desired agronomic trait, e.g. such biological properties by providing for enhanced protein activity in a transgenic plants by overexpression of the polynucleotide, e.g. with a constitutive promoter or a promoter which is active during water deficit

Protein and Polypeptide Molecules - Proteins of the present invention are whole proteins or at least a sufficient portion of the protein to impart the relevant biological activity of the protein, e.g. resistance and/or tolerance to water deficit in transgenic plants as compared to wild type, as provided by constitutive expression of the *Arabidopsis thaliana* G1073 transcription factor or a functionally homologous transcription factor. The term "protein" also includes molecules consisting of one or more polypeptide chains. Thus, a polypeptide useful in the present invention may constitute an entire gene product or one or more functional portion of a natural protein which provides the agronomic trait of this invention., i.e. enhanced yield despite exposure to water deficit.

Homologs of the polypeptides of the present invention may be identified by comparison of the amino acid sequence of the polypeptide to amino acid sequences of polypeptides from the same or different plant sources, e.g. manually or by using known homology-based search algorithms such as those commonly known and referred to as BLAST, FASTA, and Smith-Waterman.

A further aspect of the invention comprises functional homolog proteins which differ in one or more amino acids from those of a polypeptide provided herein as the result of one or more of the well-known conservative amino acid substitutions, e.g. valine is a conservative substitute for alanine and threonine is a conservative substitute for serine. Conservative substitutions for an amino acid within the native polypeptide sequence can be selected from other members of a class to which the naturally occurring amino acid belongs. Representative amino acids within these various classes include, but are not limited to: (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine. Conserved substitutes for an amino acid within a native amino acid sequence can be selected from other members of the group to which the naturally occurring amino acid belongs. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Naturally conservative amino acids substitution groups are: valine-leucine, valine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, aspartic acid-glutamic acid, and asparagine-glutamine. A further aspect of the invention comprises polypeptides which differ in one or more amino acids from those of a described protein sequence as the result of deletion or insertion of one or more amino acids in a native sequence.

Polypeptides of the present invention that are variants of the polypeptides provided herein will generally demonstrate significant identity with the polypeptides provided herein. Of particular interest are polypeptides having at least 50% sequence identity, more preferably at least about 70% sequence identity or higher, e.g. at least about 80% sequence identity with (a) an synthetic consensus amino acid sequence of SEQ ID NO:11 or (b) a conserved amino acid region of SEQ ID NO: 7 through 10 or (c) an amino acid sequence of SEQ ID NO:1 through 3, or (d) other functional homologs of any polypeptide identified in (a) through (c). Of course useful

polypeptides also include those with higher identity to such a polypeptide sequence, e.g. 90%, to 100% identity. Other polypeptides of interest have at least 50 or more, e.g. at least 60 or 70 of the amino acids of a conserved segment of the transcription factors proteins as defined by SEQ ID NO:7 through 10 and the synthetic consensus amino acid sequence of SEQ ID NO:11. Of course useful polypeptides also include those with higher percentage of the amino acids in an protein segment of SEQ ID NO:7 thorough 11.

Recombinant DNA Constructs - The present invention contemplates the use of polynucleotides which encode a protein effective for imparting resistance and/or tolerance to water deficit in plants. Such polynucleotides are assembled in recombinant DNA constructs using methods known to those of ordinary skill in the art. A useful technology for building DNA constructs and vectors for transformation is the GATEWAY™ cloning technology (available from Invitrogen Life Technologies, Carlsbad, California) uses the site specific recombinase LR cloning reaction of the Integrase/*att* system from bacterophage lambda vector construction, instead of restriction endonucleases and ligases. The LR cloning reaction is disclosed in U.S. Patents 5,888,732 and 6,277,608, U.S. Patent Application Publications 2001283529, 2001282319 and 20020007051, all of which are incorporated herein by reference. The GATEWAY™ Cloning Technology Instruction Manual which is also supplied by Invitrogen also provides concise directions for routine cloning of any desired RNA into a vector comprising operable plant expression elements.

Transgenic DNA constructs used for transforming plant cells will comprise the heterologous DNA which one desires to introduced into and a promoter to express the heterologous DNA in the host maize cells. As is well known in the art such constructs typically also comprise a promoter and other regulatory elements, 3' untranslated regions (such as polyadenylation sites), transit or signal peptides and marker genes elements as desired. For instance, see U.S. Patents No. 5,858,642 and 5,322,938which disclose versions of the constitutive promoter derived from cauliflower mosaic virus (CaMV35S), U.S. Patent 6,437,217 which discloses a maize RS81 promoter, U.S. Patent 5,641,876 which discloses a rice actin promoter, U.S. Patent 6,426,446 which discloses a maize RS324 promoter, U.S. Patent 6,429,362 which discloses a maize PR-1 promoter, U.S. Patent 6,232,526 which discloses a maize A3 promoter, U.S. Patent 6,177,611 which discloses constitutive maize promoters, U.S. Patent 6,433,252 which discloses a maize L3 oleosin promoter, U.S. Patent 6,429,357 which

discloses a rice actin 2 promoter and intron, U.S. Patent 5,837,848 which discloses a root specific promoter, U.S. Patent 6,084,089 which discloses cold inducible promoters, U.S. Patent 6,294,714 which discloses light inducible promoters, U.S. Patent 6,140,078 which discloses salt inducible promoters, U.S. Patent 6,252,138 which discloses pathogen inducible promoters, U.S. Patent 6,175,060 which discloses phosphorus deficiency inducible promoters, U.S. Patent Application Publication 2002/0192813A1 which discloses 5', 3' and intron elements useful in the design of effective plant expression vectors, U.S. patent application Serial No. 09/078,972 which discloses a coixin promoter, U.S. patent application Serial No. 09/757,089 which discloses a maize chloroplast aldolase promoter, all of which are incorporated herein by reference.

In many aspects of the invention it is preferred that the promoter element in the DNA construct should be capable of causing sufficient expression to result in the production of an effective amount of the transcription factor in water deficit conditions. Such promoters can be identified and isolated from the regulatory region of plant genes which are over expressed in water deficit conditions. Specific water-deficit-inducible promoters for use in this invention are derived from the 5' regulatory region of genes identified as a heat shock protein 17.5 gene (*HSP17.5)*, an HVA22 gene *(HVA22)*, and a cinnamic acid 4-hydroxylase (CA4H) gene *(CA4H)* of *Zea maize*. Such water-deficit-inducible promoters are disclosed in U.S. provisional application Serial No. 60/435,987, filed December 20, 2002, incorporated herein by reference.

In general it is preferred to introduce heterologous DNA randomly, i.e. at a non-specific location, in the plant genome. In special cases it may be useful to target heterologous DNA insertion in order to achieve site specific integration, e.g. to replace an existing gene in the genome. In some other cases it may be useful to target a heterologous DNA integration into the genome at a predetermined site from which it is known that gene expression occurs. Several site specific recombination systems exist which are known to function implants include cre-lox as disclosed in U.S. Patent 4,959,317 and FLP-FRT as disclosed in U.S. Patent 5,527,695, both incorporated herein by reference.

Constructs and vectors may also include a transit peptide for targeting of a gene target to a plant organelle, particularly to a chloroplast, leucoplast or other plastid organelle. For a description of the use of a chloroplast transit peptide see U.S. Patent 5, 188,642, incorporated herein by reference.

In practice DNA is introduced into only a small percentage of target cells in any one experiment. Marker genes are used to provide an efficient system for identification of those cells that are stably transformed by receiving and integrating a transgenic DNA construct into their genomes. Preferred marker genes provide selective markers which confer resistance to a selective agent, such as an antibiotic or herbicide. Potentially transformed cells are exposed to the selective agent. In the population of surviving cells will be those cells where, generally, the resistance-conferring gene has been integrated and expressed at sufficient levels to permit cell survival. Cells may be tested further to confirm stable integration of the exogenous DNA. Useful selective marker genes include those conferring resistance to antibiotics such as kanamycin (*nptII*), hygromycin B (*aph IV*) and gentamycin (*aac3* and *aac*C4) or resistance to herbicides such as glufosinate (*bar* or *pat*) and glyphosate (EPSPS). Examples of such selectable are illustrated in U.S. Patents 5,550,318; 5,633,435; 5,780,708 and 6,118,047, all of which are incorporated herein by reference. Screenable markers which provide an ability to visually identify transformants can also be employed, *e.g.*, a gene expressing a colored or fluorescent protein such as a luciferase or green fluorescent protein (GFP) or a gene expressing a *beta*-glucuronidase or *uid*A gene (GUS) for which various chromogenic substrates are known.

Transformation Methods and Transgenic Plants - Methods and compositions for transforming plants by introducing a transgenic DNA construct into a plant genome in the practice of this invention can include any of the well-known and demonstrated methods. Preferred methods of plant transformation are microprojectile bombardment as illustrated in U.S. Patents 5,015,580; 5,550,318; 5,538,880; 6,160,208; 6,399,861 and 6,403,865 and *Agrobacterium*-mediated transformation as illustrated in U.S. Patents 5,635,055; 5,824,877; 5,591,616; 5,981,840 and 6,384,301, all of which are incorporated herein by reference. See also U.S. application Serial No. 09/823,676, incorporated herein by reference, for a description of vectors, transformation methods, and production of transformed *Arabidopsis thaliana* plants where transcription factors such as G1073 are constitutively expressed by a CaMV35S promoter.

Transformation methods of this invention to provide plants with enhanced environmental stress tolerance are preferably practiced in tissue culture on media and in a controlled environment. "Media" refers to the numerous nutrient mixtures that are used to grow cells *in vitro*, that is, outside of the intact living organism. Recipient cell targets include, but are not limited to, meristem cells, callus, immature embryos and gametic cells such as microspores,

pollen, sperm and egg cells. It is contemplated that any cell from which a fertile plant may be regenerated is useful as a recipient cell. Callus may be initiated from tissue sources including, but not limited to, immature embryos, seedling apical meristems, microspores and the like. Those cells which are capable of proliferating as callus also are recipient cells for genetic transformation. Practical transformation methods and materials for making transgenic plants of this invention, e.g. various media and recipient target cells, transformation of immature embryos and subsequent regeneration of fertile transgenic plants are disclosed in U.S. Patent 6,194,636 and U.S. patent application Serial No. 09/757,089, which are incorporated herein by reference.

The seeds of this invention can be harvested from fertile transgenic plants and be used to grow progeny generations of transformed plants of this invention including hybrid plants line comprising the DNA construct expressing a transcription factor which provides the benefits of resistance and/or tolerance to water deficit.

Breeding of Transgenic Plants

In addition to direct transformation of a plant with a recombinant DNA construct, transgenic plants can be prepared by crossing a first plant having a recombinant DNA construct with a second plant lacking the construct. For example, recombinant DNA can be introduced into a plant line that is amenable to transformation to produce a transgenic plant which can be crossed with a second plant line to introgress the recombinant DNA into the second plant line.

In one aspect of the invention a transgenic plant with recombinant DNA conferring a crop improvement trait is crossed with a transgenic plant having recombinant DNA conferring herbicide and/or pest resistance to produce progeny plants having recombinant DNA that confers both the crop improvement trait and the herbicide and/or pest resistance trait. Preferably, in such breeding for combining traits the transgenic plant donating the crop improvement trait is a female line and the transgenic plant donating the herbicide and/or pest resistance trait is a male line. The progeny of this cross will segregate such that some of the plant will carry the DNA for both parental traits and some will carry DNA for one parental trait; such plants can be identified by markers associated with parental recombinant DNA Progeny plants carrying DNA for both parental traits can be crossed back into the female parent line multiple times, e.g. usually 6 to 8 generations, to produce a progeny plant with substantially the same genotype as one original transgenic parental line but for the recombinant DNA of the other transgenic parental line.

In yet another aspect of the invention hybrid transgenic seed, e.g. a hybrid transgenic corn seed, is produced by crossing a female transgenic corn line containing recombinant DNA conferring a crop improvement trait with a male transgenic corn line containing recombinant DNA conferring herbicide and/or pest resistance. In a preferred aspect of this invention hybrid transgenic corn seed is produced by crossing a female transgenic corn line with recombinant DNA conferring both a crop improvement trait and herbicide resistance with a male transgenic corn line with recombinant DNA conferring both herbicide resistance and pest resistance.

Having now generally described the invention, the same will be more readily understood through reference to the following example which is provided by way of illustration, and is not intended to be limiting of the present invention, unless specified.

Examples

These examples illustrates the use of a polynucleotide encoding transcription factor G1073 to provide a transgenic plant exhibiting enhanced tolerance for and/or resistance to growing conditions of water deficit.

Transgenic *Arabidopsis thaliana* was prepared with an exogenous DNA construct comprising a constitutive promoter of CaMV 35S operably linked to a polynucleotide of SEQ ID NO: 12 encoding *Arabidopsis thaliana* transcription factor G1073 of SEQ ID NO:1. Transgenic and wild type plants were potted in garden soil in a controlled environmental growth chamber in a 12hour light/dark cycle. When the plants were at the early flowering stage, they were screened for water-deficit tolerance. Water was withheld until the wild type plants began wilting. Carbon dioxide assimilation rates were measured at growth and saturated conditions. Growth conditions were light at 200 μmol m^{-2} s^{-1} and 350 ppm CO_2. Saturating conditions were light at 1000 μmol m^{-2} s^{-1} and 1000 ppm CO_2. Wild type plants had smaller stomata conductance and lower CO_2 assimilation rates than did the transgenic plants.

Transgenic soybean was prepared with an exogenous DNA construct comprising a constitutive promoter CaMV35S operably linked to a polynucleotide of SEQ ID NO: 12 encoding *Arabidopsis thaliana* transcription factor G1073 of SEQ ID NO:1. When grown in water-deficit assay conditions the transgenic soybean showed enhanced resistance and/or tolerance to water deficit as compared to wild type.

Transgenic corn was prepared with an exogenous DNA construct comprising a constitutive promoter of the rice actin 1 gene operably linked to a polynucleotide of SEQ ID NO:

12 encoding *Arabidopsis thaliana* transcription factor G1073 of SEQ ID NO:1. Transgenic corn exhibited various enhance traits, e.g. increased biomass, increased seed oil, increased yield and the ability to utilize high levels of nitrogen.

5